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RAW SEQUENCE LISTING DATE: 07/24/2001 PATENT APPLICATION: US/09/904,954 TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt
Output Set: N:\CRF3\07242001\1904954.raw

SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
             (i) APPLICANT: BECKMANN, M. P.
      6
      7
                            CERRETTI, DOUGLAS P.
      9
            (ii) TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
     10
                                     RECEPTOR HEK
     12
           (iii) NUMBER OF SEQUENCES: 4
            (iv) CORRESPONDENCE ADDRESS:
     14
     15
                  (A) ADDRESSEE: IMMUNEX CORPORATION
                                                                ENTERED
     16
                  (B) STREET: 51 UNIVERSITY STREET
     17
                  (C) CITY: SEATTLE
                  (D) STATE: WASHINGTON
     18
                  (E) COUNTRY: USA
     19
                  (F) ZIP: 98101
     20
             (V) COMPUTER READABLE FORM:
     22
     23
                  (A) MEDIUM TYPE: Floppy disk
                  (B) COMPUTER: Apple Macintosh
     24
     25
                  (C) OPERATING SYSTEM: Apple System 7.1
                  (D) SOFTWARE: Microsoft Word for Apple, Version 5.1a
     26
            (vi) CURRENT APPLICATION DATA:
     28
                  (A) APPLICATION NUMBER: US/09/904,954
C--> 29
                  (B) FILING DATE: 12-Jul-2001
C--> 30
     31
                  (C) CLASSIFICATION:
           (vii) PRIOR APPLICATION DATA:
     41
                  (A) APPLICATION NUMBER: 08/240,124
     34
     35
                  (B) FILING DATE:
     38
                  (A) APPLICATION NUMBER: US 08/114,426
     39
                 (B) FILING DATE: 30-AUG-1993
                  (A) APPLICATION NUMBER: US 08/109,745
     42
                  (B) FILING DATE: 20-AUG-1993
     43
     45
          (viii) ATTORNEY/AGENT INFORMATION:
     46
                  (A) NAME: SEESE, KATHRYN A.
     47
                  (B) REGISTRATION NUMBER: 32,172
                  (C) REFERENCE/DOCKET NUMBER: 2814-C
     48
            (ix) TELECOMMUNICATION INFORMATION:
     50
     51
                  (A) TELEPHONE: (206) 587-0430
                  (B) TELEFAX: (206) 233-0644
     52
                  (C) TELEX: 756822
     56 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
    58
    59
                  (A) LENGTH: 1037 base pairs
     60
                  (B) TYPE: nucleic acid
    61
                  (C) STRANDEDNESS: single
    62
                  (D) TOPOLOGY: linear
    64
            (ii) MOLECULE TYPE: cDNA to mRNA
           (iii) HYPOTHETICAL: NO
    66
    68
            (iv) ANTI-SENSE: NO
```

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Input Set : N:\Crf3\RULE60\09904954.txt
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71 (vii) IMMEDIATE SOURCE:													
72 (B) CLONE: hek-L A2													
74 (ix) FEATURE:													
75 (A) NAME/KEY: CDS													
76 (B) LOCATION: 83799													
78 (ix) FEATURE:													
79 (A) NAME/KEY: sig_peptide 80 (B) LOCATION: 83139													
(B) LOCATION: 83139													
(ix) FEATURE:													
(A) NAME/KEY: mat_peptide													
(B) LOCATION: 140796													
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	C 0												
89 GGATCTTGGA ACGAGACGAC CTGCTGGAGA AGCCGGGAGC GCGGGGCTCA GTCGGGGGGC	60												
91 GGCGGCGGCG GCGCTCCGG GG ATG GCG GCT CCG CTG CTG CTG CTG	112												
92 Met Ala Ala Pro Leu Leu Leu Leu													
93 -19 -15 -10													
95 CTG CTC GTG CCC GTG CCG CTG CCG CTG CTG	160												
96 Leu Leu Val Pro Val Pro Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly													
97 -5 . 1 . 5													
99 GGG GCG CTG GGA AAC CGG CAT GCG GTG TAC TGG AAC AGC TCC AAC CAG	208												
100 Gly Ala Leu Gly Asn Arg His Ala Val Tyr Trp Asn Ser Ser Asn Gln													
101 10 15 20													
103 CAC CTG CGG CGA GAG GGC TAC ACC GTG CAG GTG AAC GTG AAC GAC TAT	256												
104 His Leu Arg Arg Glu Gly Tyr Thr Val Gln Val Asn Val Asn Asp Tyr													
105 25 30 35													
107 CTG GAT ATT TAC TGC CCG CAC TAC AAC AGC TCG GGG GTG GGC CCC GGG	304												
108 Leu Asp Ile Tyr Cys Pro His Tyr Asn Ser Ser Gly Val Gly Pro Gly													
109 40 45 50 55													
111 GCG GGA CCG GGG CCC GGA GGC GGG GCA GAG CAG TAC GTG CTG TAC ATG	352												
112 Ala Gly Pro Gly Pro Gly Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met													
113 60 65 70													
115 GTG AGC CGC AAC GGC TAC CGC ACC TGC AAC GCC AGC CAG GGC TTC AAG	400												
116 Val Ser Arg Asn Gly Tyr Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys													
117 75 80 85													
119 CGC TGG GAG TGC AAC CGG CCG CAC GCC CCG CAC AGC CCC ATC AAG TTC	448												
120 Arg Trp Glu Cys Asn Arg Pro His Ala Pro His Ser Pro Ile Lys Phe													
121 90 95 100													
123 TCG GAG AAG TTC CAG CGC TAC AGC GCC TTC TCT CTG GGC TAC GAG TTC	496												
124 Ser Glu Lys Phe Gln Arg Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe													
125 105 110 115													
127 CAC GCC GGC CAC GAG TAC TAC TAC ATC TCC ACG CCC ACT CAC AAC CTG	544												
128 His Ala Gly His Glu Tyr Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu													
129 120 125 130 135													
131 CAC TGG AAG TGT CTG AGG ATG AAG GTG TTC GTC TGC TGC GCC TCC ACA	592												
132 His Trp Lys Cys Leu Arg Met Lys Val Phe Val Cys Cys Ala Ser Thr													
133 140 145 150													
135 TCG CAC TCC GGG GAG AAG CCG GTC CCC ACT CTC CCC CAG TTC ACC ATG	640												
136 Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met													
137 155 160 165													

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	139	GGC	CCC	AAT	GTG	AAG	ATC	AAC	GTG	CTG	GAA	GAC	TTT	GAG	GGA	GAG	AAC	688
	140	Gly	Pro		Val	Lys	Ile	Asn		Leu	Glu	Asp	Phe		Gly	Glu	Asn	
	141			170					175					180				
			CAG															736
		Pro	Gln	Val	Pro	Lys	Leu		Lys	Ser	Ile	Ser		Thr	Ser	Pro	Lys	
	145		185					190				~~~	195		~			704
			GAA															784
		_	Glu	HIS	Leu	Pro		Ala	vaı	GIY	тте		Pne	Pne	ьeu	met		
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		Pne	Leu	Ата	ser	220												
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																	PACCCC	956
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			CGTC					IAGI	JGAC	- AA	JCAC	3000	ACA	JCCA.	IGG (31000	CONGCA	1010
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	169	· •																
	171																	
	173		•					-	ON: S	SEO I	ID NO): 2	:				•	
	175	Met	Àla		-									Val	Pro	Val	Pro	
		-19				-15					-10					-5		
	178	Leu	Leu	Pro	Leu	Leu	Ala	Gln	Gly	Pro	Gly	Gly	Ala	Leu	Gly	Asn	Arg	
	179				1				5		_	_		10				
	181	His	Ala	Val	Tyr	Trp	Asn	Ser	Ser	Asn	Gln	His	Leu	Arg	Arg	Glu	Gly	
	182		15					20					25					
	184	Tyr	Thr	Val	Gln	Val	Asn	Val	Asn	Asp	Tyr	Leu	Asp	Ile	\mathtt{Tyr}	Cys	Pro	
	185	30					35					40					45	
		His	${ t Tyr}$	Asn	Ser		Gly	Val	Gly	Pro	Gly	Ala	Gly	Pro	Gly	Pro	Gly	
	188					50					55					60		
		Gly	Gly	Ala		Gln	Tyr	Val	Leu		Met	Val	Ser	Arg		Gly	Tyr	
	191		_		65	_				70					75			
		Arg	Thr	_	Asn	Ala	Ser	Gln	_	Phe	Lys	Arg	Trp		Cys	Asn	Arg	
	194	_	•	80	_		_	_	85	_		_		90	1	-1	_	
		Pro	His	Ala	Pro	His	Ser		IIe	Lys	Phe	Ser		Lys	Phe	GIn	Arg	
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		TÀT	Tyr	тте	ser		PIO	THE	HIS	ASII		птъ	тър	гуѕ	Cys	140	AIG	
	203	Mo+	Lys	₩ a l	Dha	130	Cvc	Cvc	λ1 a	802	135	Sor	uic	Sor	G1v		T.v.c	
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	~		113					100					100					

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	Glu 190	Lys	ser	Ile	Ser	Gly 195	Thr	Ser	Pro	Lys	Arg 200	Glu	His	Leu	Pro	Leu 205	
	Ala	Val	Gly	Ile	Ala		Phe	Leu	Met	Thr		Leu	Ala	Ser			
218			1		210					215							
	1 (2) INFORMATION FOR SEQ ID NO: 3:																
223																	
224																	
225																	
226	• •																
227			(1) T(OPOLO	OGY:	line	ear									
229	9 (ii) MOLECULE TYPE: cDNA to mRNA																
231	1 (iii) HYPOTHETICAL: NO																
233	• •																
236																	
237	, ,																
239		(ix) FE	ATURI	Ξ:												
240				A) NA					tide								
241			(1	3) L(CAT:	CON:	94.	. 630									
243		(ix	•	ATURI				•									
244			•	A) NA	•												
245			•	3) LO		CON:	28.	. 633									
247		(ix	-	ATURI													
248				A) NZ			_		tide								
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252) SE	JOEN C	JE DI	iscr.	LPTIC)N: 3	SEU.	LD NU	J: 3	:					
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		AGAC	CAA A	ACCGO				CG A	rg c	GG C	rg c	rg co					51
255		AGAC	CAA A					CG A'	rg co	GG C rg Le	rg C' eu Le				eu Ai	rg	51
255 256				ACCG	GACC:	rc Go	GGGG	CG A: Me	rg co et A: 22	GG Ci rg Le	rg C' eu Le 20	IG CO eu Pi	ro Le	eu Le	eu Ai -:	rg 15	
255 256 258	ACT	GTC	CTC	ACCG(TGG	GCC	rc Go	GGGG(CG AS Me - 2 CTC	rg Co et A: 22 GGC	GG C rg Le -2 TCC	rg C' eu Le 20 CCT	TG CC eu Pi CTG	ro Le	eu Le GGG	eu Ai -: GGC	rg 15 TCC	51 99
255 256 258 259		GTC	CTC	ACCG(TGG	GACC GCC Ala	rc Go	GGGG(CG AS Me - 2 CTC	rg Co et A: 22 GGC	GG C rg Le -2 TCC Ser	rg C' eu Le 20 CCT	TG CC eu Pi CTG	ro Le	eu Le GGG	eu Ar -: GGC Gly	rg 15 TCC	
255 256 258 259 260	ACT Thr	GTC Val	CTC Leu	ACCGO TGG Trp	GACC GCC Ala -10	rc Go GCG Ala	TTC Phe	CG AS Me -2 CTC Leu	rg Co et A: 22 GGC Gly	GG C rg Le -2 TCC Ser -5	IG C' eu Le 20 CCT Pro	TG CC eu Pr CTG Leu	ro Le CGC Arg	eu Le GGG Gly	eu Ar -: GGC Gly 1	rg 15 TCC Ser	99
255 256 258 259 260 262	ACT Thr	GTC Val CTC	CTC Leu CGC	TGG Trp CAC	GACC GCC Ala -10 GTA	GCG Ala GTC	TTC Phe TAC	CG AS Me -: CTC Leu TGG	rg Co et A: 22 GGC Gly AAC	GG CT rg Le TCC Ser -5 TCC	IG C eu Le 20 CCT Pro	TG CC eu Pr CTG Leu AAC	CGC Arg	GGG Gly AGG	eu Ar - GGC Gly 1 TTG	rg 15 TCC Ser	
255 256 258 259 260 262 263	ACT Thr	GTC Val CTC	CTC Leu CGC Arg	TGG Trp CAC	GACC GCC Ala -10 GTA	GCG Ala GTC	TTC Phe TAC	CG AS Me -: CTC Leu TGG Trp	rg Co et A: 22 GGC Gly AAC	GG CT rg Le TCC Ser -5 TCC	IG C eu Le 20 CCT Pro	TG CC eu Pr CTG Leu AAC	CGC Arg CCC Pro	GGG Gly AGG	eu Ar - GGC Gly 1 TTG	rg 15 TCC Ser	99
255 256 258 259 260 262 263 264	ACT Thr AGC Ser	GTC Val CTC Leu	CTC Leu CGC Arg 5	TGG Trp CAC	GCC Ala -10 GTA Val	GCG Ala GTC Val	TTC Phe TAC Tyr	CG AS MG -: CTC Leu TGG Trp 10	rg Coet A: 22 GGC Gly AAC Asn	GG CT rg Le -2 TCC Ser -5 TCC Ser	IG C eu Le 20 CCT Pro AGT Ser	TG CC eu Pr CTG Leu AAC Asn	CGC Arg CCC Pro 15	GGG Gly AGG Arg	eu Ar -: GGC Gly 1 TTG Leu	rg 15 TCC Ser CTT Leu	99
255 256 258 259 260 262 263 264 266	ACT Thr AGC Ser	GTC Val CTC Leu GGA	CTC Leu CGC Arg 5 GAC	TGG Trp CAC His	GCC Ala -10 GTA Val	GCG Ala GTC Val	TTC Phe TAC Tyr	CG AT MG -7 CTC Leu TGG Trp 10 CTG	rg Coet A: 22 GGC Gly AAC Asn	GG CT rg Le -7 TCC Ser -5 TCC Ser	IG C eu Le 20 CCT Pro AGT Ser	CTG CTG Leu AAC Asn GAT	CGC Arg CCC Pro 15	GGG Gly AGG Arg	GGC Gly TTG Leu GAC	rg 15 TCC Ser CTT Leu	99 147
255 256 258 259 260 262 263 264 266 267	ACT Thr AGC Ser	GTC Val CTC Leu GGA Gly	CTC Leu CGC Arg 5 GAC	TGG Trp CAC His	GCC Ala -10 GTA Val	GCG Ala GTC Val	TTC Phe TAC Tyr	CG AT MG -7 CTC Leu TGG Trp 10 CTG	rg Coet A: 22 GGC Gly AAC Asn	GG CT rg Le -7 TCC Ser -5 TCC Ser	IG C eu Le 20 CCT Pro AGT Ser	CTG CTG Leu AAC Asn GAT	CGC Arg CCC Pro 15	GGG Gly AGG Arg	GGC Gly TTG Leu GAC	rg 15 TCC Ser CTT Leu	99 147
255 256 258 259 260 262 263 264 266 267 268	ACT Thr AGC Ser CGA Arg	GTC Val CTC Leu GGA Gly 20	CTC Leu CGC Arg 5 GAC Asp	TGG Trp CAC His GCC Ala	GCC Ala -10 GTA Val GTG Val	GCG Ala GTC Val GTG Val	TTC Phe TAC Tyr GAG Glu 25	CG AM Me CTC Leu TGG Trp 10 CTG Leu	GC GLY AAC ASD GGC GLY	TCC Ser -5 TCC Ser -5 TCC Ser CTC	IG CT eu Le 20 CCT Pro AGT Ser AAC Asn	CTG Leu AAC Asn GAT Asp 30	CGC Arg CCC Pro 15 TAC	GGG Gly AGG Arg CTA Leu	GGC Gly TTG Leu GAC Asp	rg 15 TCC Ser CTT Leu ATT	99 147
255 256 258 259 260 262 263 264 266 267 268 270	ACT Thr AGC Ser	GTC Val CTC Leu GGA Gly 20 TGC	CTC Leu CGC Arg 5 GAC Asp	TGG Trp CAC His GCC Ala	GCC Ala -10 GTA Val GTG Val	GCG Ala GTC Val GTG Val	TTC Phe TAC Tyr GAG Glu 25 GGC	CG AS Me -2 CTC Leu TGG Trp 10 CTG Leu	GC GLY AAC ASD GGC GLY GGC GLY	TCC Ser -5 TCC Ser -5 TCC Ser CTC Leu	IG CT eu Le 20 CCT Pro AGT Ser AAC ASn CCT	CTG Leu AAC Asn GAT Asp 30 GAG	CGC Arg CCC Pro 15 TAC Tyr GGC	GGG Gly AGG Arg CTA Leu	GGC Gly TTG Leu GAC Asp	rg 15 TCC Ser CTT Leu ATT Ile	99 147 195
255 256 258 259 260 262 263 264 266 267 268 270	ACT Thr AGC Ser CGA Arg GTC Val	GTC Val CTC Leu GGA Gly 20 TGC	CTC Leu CGC Arg 5 GAC Asp	TGG Trp CAC His GCC Ala	GCC Ala -10 GTA Val GTG Val	GCG Ala GTC Val GTG Val	TTC Phe TAC Tyr GAG Glu 25 GGC Gly	CG AS Me -2 CTC Leu TGG Trp 10 CTG Leu	GGC GLY GGC GLY GGC GLY GGC GLY GGG GLY	TCC Ser -5 TCC Ser -5 TCC Ser CTC Leu	IG C'eu Le 20 CCT Pro AGT Ser AAC ASn CCT	CTG Leu AAC Asn GAT Asp GAG GAG	CGC Arg CCC Pro 15 TAC Tyr GGC	GGG Gly AGG Arg CTA Leu	GGC Gly TTG Leu GAC Asp	rg 15 TCC Ser CTT Leu ATT Ile	99 147 195
255 258 259 260 262 263 264 266 267 268 270 271	ACT Thr AGC Ser CGA Arg GTC Val 35	GTC Val CTC Leu GGA Gly 20 TGC Cys	CTC Leu CGC Arg 5 GAC Asp CCC Pro	TGG Trp CAC His GCC Ala CAC	GCC Ala -10 GTA Val GTG Val	GCG Ala GTC Val GTG Val GAA Glu 40	TTC Phe TAC Tyr GAG Glu 25 GGC Gly	CG A' MG -: CTC Leu TGG Trp 10 CTG Leu CCA Pro	GGC ASD GGC Gly GGC Gly GGC Gly GGC Gly	TCC Ser -5 TCC Ser -5 TCC Ser CTC Leu CCC Pro	IG C'eu Le 20 CCT Pro AGT Ser AAC ASD CCT Pro 45	CTG Leu AAC Asn GAT Asp GAG GAG	CGC Arg CCC Pro 15 TAC Tyr GGC Gly	GGG Gly AGG Arg CTA Leu CCC Pro	GGC Gly 1 TTG Leu GAC Asp GAG Glu	TCC Ser CTT Leu ATT Ile ACG Thr 50	99 147 195
255 258 259 260 262 263 264 266 267 268 270 271 272 274	ACT Thr AGC Ser CGA Arg GTC Val 35	GTC Val CTC Leu GGA Gly 20 TGC Cys	CTC Leu CGC Arg 5 GAC Asp CCC Pro	TGG Trp CAC His GCC Ala CAC His	GCC Ala -10 GTA Val GTG Val TAC Tyr	GCG Ala GTC Val GTG Val GAA Glu 40 GTG	TTC Phe TAC Tyr GAG Glu 25 GGC Gly	CG A' MG -: CTC Leu TGG Trp 10 CTG Leu CCA Pro	GC GLY GGC GLY GGC GLY GGC GLY GGC GLY GGC GLY	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro	IG C'eu Le 20 CCT Pro AGT Ser AAC ASD CCT Pro 45	CTG Leu AAC Asn GAT Asp 30 GAG Glu GAG	CGC Arg CCC Pro 15 TAC Tyr GGC Gly	GGG Gly AGG Arg CTA Leu CCC Pro	GGC Gly 1 TTG Leu GAC Asp GAG Glu CAG	TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA	99 147 195 243
255 258 259 260 262 263 264 266 270 271 272 274	ACT Thr AGC Ser CGA Arg GTC Val 35	GTC Val CTC Leu GGA Gly 20 TGC Cys	CTC Leu CGC Arg 5 GAC Asp CCC Pro	TGG Trp CAC His GCC Ala CAC His	GCC Ala -10 GTA Val GTG Val TAC Tyr	GCG Ala GTC Val GTG Val GAA Glu 40 GTG	TTC Phe TAC Tyr GAG Glu 25 GGC Gly	CG A' MG -: CTC Leu TGG Trp 10 CTG Leu CCA Pro	GC GLY GGC GLY GGC GLY GGC GLY GGC GLY GGC GLY	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro	IG C'eu Le 20 CCT Pro AGT Ser AAC ASD CCT Pro 45	CTG Leu AAC Asn GAT Asp 30 GAG Glu GAG	CGC Arg CCC Pro 15 TAC Tyr GGC Gly	GGG Gly AGG Arg CTA Leu CCC Pro	GGC Gly 1 TTG Leu GAC Asp GAG Glu CAG	TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA	99 147 195 243
255 258 259 260 262 263 264 266 270 271 272 274 275 276	ACT Thr AGC Ser CGA Arg GTC Val 35	GTC Val CTC Leu GGA Gly 20 TGC Cys	CTC Leu CGC Arg 5 GAC Asp CCC Pro	TGG Trp CAC His GCC Ala CAC His	GCC Ala -10 GTA Val GTG Val TAC Tyr ATG Met 55	GCG Ala GTC Val GTG Val GAA Glu 40 GTG Val	TTC Phe TAC Tyr GAG Glu 25 GGC Gly GAC Asp	CG A' MG -: CTC Leu TGG Trp 10 CTG Leu CCA Pro TGG Trp	GGC Gly AAC Asn GGC Gly GGG Gly CCA Pro	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro GGC Gly 60	IG CT Pro AGT Ser AAC Asn CCT Pro 45 TAT	CTG Leu AAC Asn GAT Asp GAG Glu GAG Glu	CGC Arg CCC Pro 15 TAC Tyr GGC Gly TCC Ser	GGG Gly AGG Arg CTA Leu CCC Pro	GGC Gly 1 TTG Leu GAC Asp GAG Glu CAG Gln 65	rg 15 TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA Ala	99 147 195 243
255 258 259 260 262 263 264 266 270 271 272 274 275 276 278	ACT Thr AGC Ser CGA Arg GTC Val 35 TTT Phe	GTC Val CTC Leu GGA Gly 20 TGC Cys GCT Ala	CTC Leu CGC Arg 5 GAC Asp CCC Pro TTG Leu	TGG Trp CAC His GCC Ala CAC His	GCC Ala -10 GTA Val GTG Val TAC TYr ATG Met 55 GCC	GCG Ala GTC Val GTG Val GAA Glu 40 GTG Val	TTC Phe TAC Tyr GAG Glu 25 GGC Gly GAC Asp	CG A' MG -: CTC Leu TGG Trp 10 CTG Leu CCA Pro TGG Trp	GC Gly AAC Asn GGC Gly GGG Gly CCA Pro	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro GGC Gly 60 GTG	IG CT Pro AGT Ser AAC Asn CCT Pro 45 TAT Tyr	CTG Leu AAC Asn GAT Asp 30 GAG Glu GAG Glu TCC	CGC Arg CCC Pro 15 TAC Tyr GGC Gly TCC Ser	GGG Gly AGG Arg CTA Leu CCC Pro TGC Cys	GGC Gly TTG Leu GAC Asp GAG Glu CAG Gln 65	rg 15 TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA Ala	99 147 195 243 291
255 258 259 260 262 263 264 266 267 272 274 275 276 278 279 280	ACT Thr AGC Ser CGA Arg GTC Val 35 TTT Phe GAG Glu	GTC Val CTC Leu GGA Gly 20 TGC Cys GCT Ala GGC Gly	CTC Leu CGC Arg 5 GAC Asp CCC Pro TTG Leu CCC	TGG Trp CAC His GCC Ala CAC His TAC Tyr CGG Arg	GCC Ala -10 GTA Val GTG Val ATG Met 55 GCC Ala	GCG Ala GTC Val GTG Val GAA Glu 40 GTG Val TAC	TTC Phe TAC Tyr GAG Glu 25 GGC Gly GAC Asp AAG Lys	CG A' MG -: CTC Leu TGG Trp 10 CTG Leu CCA Pro TGG Trp CGC Arg	GC Gly AAC Asn GGC Gly CCA Pro TGG Trp 75	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro GGC Gly 60 GTG Val	IG C'eu Le 20 CCT Pro AGT Ser AAC Asn CCT Pro 45 TAT Tyr	CTG Leu AAC Asn GAT Asp 30 GAG Glu GAG Glu TCC Ser	CGC Arg CCC Pro 15 TAC Tyr GGC Gly TCC Ser CTG Leu	GGG Gly AGG Arg CTA Leu CCC Pro TGC Cys CCC Pro 80	GGC Gly TTG Leu GAC Asp GAG Glu CAG Gln 65 TTT Phe	TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA Ala GGC Gly	99 147 195 243 291 339
255 258 259 260 262 263 264 266 267 271 272 274 275 276 278 279 280 282	ACT Thr AGC Ser CGA Arg GTC Val 35 TTT Phe GAG Glu	GTC Val CTC Leu GGA Gly 20 TGC Cys GCT Ala GGC Gly	CTC Leu CGC Arg 5 GAC Asp CCC Pro TTG Leu CCC Pro	TGG Trp CAC His GCC Ala CAC His TAC Tyr CGG Arg 70	GCC Ala -10 GTA Val GTG Val ATG Met 55 GCC Ala TCA	GCG Ala GTC Val GTG Val GAA Glu 40 GTG Val TAC Tyr	TTC Phe TAC Tyr GAG Glu 25 GGC Gly GAC Asp AAG Lys	CG A' MG CTC Leu TGG Trp 10 CTG Leu CCA Pro TGG Trp CGC Arg	GC Gly AAC Asn GGC Gly GGG Gly CCA Pro TGG Trp 75 CAG	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro GGC Gly 60 GTG Val	IG C'eu Le 20 CCT Pro AGT Ser AAC Asn CCT Pro 45 TAT Tyr TGC Cys	CTG Leu AAC Asn GAT Asp 30 GAG Glu GAG Glu TCC Ser	CGC Arg CCC Pro 15 TAC Tyr GGC Gly TCC Ser CTG Leu CCT	GGG Gly AGG Arg CTA Leu CCC Pro TGC Cys CCC Pro 80 TTC	GGC Gly TTG Leu GAC Asp GAG Glu CAG Gln 65 TTT Phe	TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA Ala GGC Gly CTC	99 147 195 243 291
255 258 259 260 262 263 264 266 267 271 272 274 275 276 278 279 280 282	ACT Thr AGC Ser CGA Arg GTC Val 35 TTT Phe GAG Glu	GTC Val CTC Leu GGA Gly 20 TGC Cys GCT Ala GGC Gly	CTC Leu CGC Arg 5 GAC Asp CCC Pro TTG Leu CCC Pro	TGG Trp CAC His GCC Ala CAC His TAC Tyr CGG Arg 70	GCC Ala -10 GTA Val GTG Val ATG Met 55 GCC Ala TCA	GCG Ala GTC Val GTG Val GAA Glu 40 GTG Val TAC Tyr	TTC Phe TAC Tyr GAG Glu 25 GGC Gly GAC Asp AAG Lys	CG A' MG CTC Leu TGG Trp 10 CTG Leu CCA Pro TGG Trp CGC Arg	GC Gly AAC Asn GGC Gly GGG Gly CCA Pro TGG Trp 75 CAG	GG CT TCC Ser -5 TCC Ser CTC Leu CCC Pro GGC Gly 60 GTG Val	IG C'eu Le 20 CCT Pro AGT Ser AAC Asn CCT Pro 45 TAT Tyr TGC Cys	CTG Leu AAC Asn GAT Asp 30 GAG Glu GAG Glu TCC Ser	CGC Arg CCC Pro 15 TAC Tyr GGC Gly TCC Ser CTG Leu CCT	GGG Gly AGG Arg CTA Leu CCC Pro TGC Cys CCC Pro 80 TTC	GGC Gly TTG Leu GAC Asp GAG Glu CAG Gln 65 TTT Phe	TCC Ser CTT Leu ATT Ile ACG Thr 50 GCA Ala GGC Gly CTC	99 147 195 243 291 339

RAW SEQUENCE LISTING DATE: 07/24/2001 PATENT APPLICATION: US/09/904,954 TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt
Output Set: N:\CRF3\07242001\1904954.raw

		TTT															435
287	Gly	Phe	Glu	Phe	Leu	Pro	-	Glu	Thr	\mathtt{Tyr}	Tyr	Tyr	Ile	Ser	Val	Pro	
288		100					105					110				•	
		CCA															483
		Pro	Glu	Ser	Ser	_	Gln	Cys	Leu	Arg		Gln	Val	Ser	Val	_	
	115					120					125					130	
		AAG															531
	Cys	Lys	Glu	Arg		Ser	GLu	Ser	Ala		Pro	Val	GLY	ser		GLY	
296	a. a	3.00	000		135	000	maa	003	000	140	010	3 CM	000	3.00	145	ama.	E 7.0
		AGT															579
	GIU	Ser	СТУ	150	ser	СТА	ттр	Arg	155	GIY	ASP	THE	PIO	160	PIO	Leu	
300	ጥርጥ	CTC	ጥጥሮ		מיחיז.	CTC	CTC	CTT		አ ጥጥ	CTT	CCT	COTO		CGA	አ ጥጥ	627
		Leu	*														027
304	Суз	пеа	165	пец	неи	пеа	пец	170	пец	116	цец	Arg	175	пеа	nry	116	
	CTG	TGAC						1/0					1/3				636
	Leu	IOA	JCC			•											050
308	ЦСИ	180															
	(2)	INFO	ראאז	מסדיו	FOR	SEO	TD N	10 · 4	1 •								
314				QUENC													
315		(-/		A) LI						ls							
316			-	3) TY													
317			•	•													
319		(D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein															
321		(xi)	SEC	QUENC	E DI	ESCR	PTIC	ON: 5	SEQ]	D NO): 4:	:					
323	Met	Arg	Leu	Leu	Pro	Leu	Leu	Arg	Thr	Val	Leu	Trp	Ala	Ala	Phe	Leu	
	-22		-20					-15					-10				
326	Gly	Ser	Pro	Leu	Arg	Gly	Gly	Ser	Ser	Leu	Arg	His	Val	Val	Tyr	Trp	
327		- 5					1				5					10	
	Asn	Ser	Ser	Asn	Pro	Arg	Leu	Leu	Arg	Gly	Asp	Ala	Val	Val	Glu	Leu	
330					15	•				20					25		
	Gly	Leu	Asn		Tyr	Leu	Asp	Ile		Cys	Pro	His	Tyr		Gly	Pro	
333			_	30		_			35		_	_		40		_	
	Gly	Pro		Glu	Gly	Pro	Glu		Phe	Ala	Leu	Tyr		Val	Asp	Trp	
336	_	~ 3	45	a 3			~ 1	50			_	_	55	_	_	_	
	Pro	Gly	Tyr	GIu	Ser	Cys		Ата	GLu	GIY	Pro		Ala	Tyr	Lys	Arg	
339	m	60	0	C	T	D	65 Dha	G1	TT 4 -	37-1	a 1	70 Dha	, G	61	T	T1.	
	75	Val	Cys	ser	ren		Pne	GTA	HIS	vaı		Pne	ser	GIU	гàг		
342		Arg	Dho		Dro	80 Dho	Cor	T 011	C1.,	Dho	85 (21)	Dho	Tou	Dro	C111	90	
345	GIII	MIG	FILE	1111	95	rne	Ser	пеп	СТУ	100	GIU	FIIE	ьеu	PIO	105	GIU	
	Thr	Tyr	ጥላሪዮ	ጥኒኒዮ		Sor	Va l	Dro	Thr		Glu	Ser	Sar	G1v		Cve	
348	T 111	тут	тут	110	TIE	Ser	Val	FIO	1115	FIO	Gru	Ser	Set	120	GIII	Cys	
	Len	Arg	Len		Val	Ser	Val	Cvs		Lvs	Glu	Arσ	Lvg		Glu	Ser	
351	_cu	-11-9	125	O 7 11	, 41	501	+ u. i.	130	010	273	JIU	9	135	JC1	JIU	501	
	Ala	His		Val	Glv	Ser	Pro	-	Glu	Ser	Glv	Thr		G1v	Trp	Ara	
354		140			1		145	1			1	150		1	F	9	
	Gly	Gly	Asp	Thr	Pro	Ser		Leu	Cys	Leu	Leu		Leu	Leu	Leu	Leu	
357		_	•			160			-		165					170	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001 TIME: 11:32:59

Input Set : N:\Crf3\RULE60\09904954.txt
Output Set: N:\CRF3\07242001\1904954.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1 L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3